

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: DUAN, ROXANNE
RUBEN, STEVEN

(ii) TITLE OF INVENTION: Parotid Secretory Protein

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
(B) STREET: 9410 KEY WEST AVENUE
(C) CITY: ROCKVILLE
(D) STATE: MD
(E) COUNTRY: US
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROOKES, ANDERS A.
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PF348

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1028 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 49..795

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 49..100

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 103..795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGAGATT CATGAGCATC CTCCTCTAAA CGCGTGTCAA GACAAAAG ATG CTT CAG
Met Leu Gln

5	CTT TGG AAA CTT GTT CTC CTG TGC GGC GTG CTC ACT GGG ACC TCA GAG Leu Trp Lys Leu Val Leu Leu Cys Gly Val Leu Thr Gly Thr Ser Glu -15 -10 -5 1	105
10	TCT CTT CTT GAC AAT CTT GGC AAT GAC CTA AGC AAT GTC GTG GAT AAG Ser Leu Leu Asp Asn Leu Gly Asn Asp Leu Ser Asn Val Val Asp Lys 5 10 15	153
15	CTG GAA CCT GTT CTT CAC GAG GGA CTT GAG ACA GTT GAC AAT ACT CTT Leu Glu Pro Val Leu His Glu Gly Leu Glu Thr Val Asp Asn Thr Leu 20 25 30	201
20	AAA GGC ATC CTT GAG AAA CTG AAG GTC GAC CTA GGA GTG CTT CAG AAA Lys Gly Ile Leu Glu Lys Leu Lys Val Asp Leu Gly Val Leu Gln Lys 35 40 45	249
25	TCC AGT GCT TGG CAA CTG GCC AAG CAG AAG GCC CAG GAA GCT GAG AAA Ser Ser Ala Trp Gln Leu Ala Lys Gln Lys Ala Gln Glu Ala Glu Lys 50 55 60 65	297
30	TTG CTG AAC AAT GTG ATT TCT AAG CTG CTT CCA ACT AAC ACG GAC ATT Leu Leu Asn Asn Val Ile Ser Lys Leu Leu Pro Thr Asn Thr Asp Ile 70 75 80	345
35	TTT GGG TTG AAA ATC AGC AAC TCC CTC ATC CTG GAT GTC AAA GCT GAA Phe Gly Leu Lys Ile Ser Asn Ser Leu Ile Leu Asp Val Lys Ala Glu 85 90 95	393
40	CCG ATC GAT GAT GGC AAA GGC CTT AAC CTG AGC TTC CCT GTC ACC GCG Pro Ile Asp Asp Gly Lys Gly Leu Asn Leu Ser Phe Pro Val Thr Ala 100 105 110	441
45	AAT GTC ACT GTG GCC GGG CCC ATC ATT GGC CAG ATT ATC AAC CTG AAA Asn Val Thr Val Ala Gly Pro Ile Ile Gly Gln Ile Ile Asn Leu Lys 115 120 125	489
50	GCC TCC TTG GAC CTC CTG ACC GCA GTC ACA ATT GAA ACT GAT CCC CAG Ala Ser Leu Asp Leu Leu Thr Ala Val Thr Ile Glu Thr Asp Pro Gln 130 135 140 145	537
55	ACA CAC CAG CCT GTT GCC GTC CTG GGA GAA TGC GCC AGT GAC CCA ACC Thr His Gln Pro Val Ala Val Leu Gly Glu Cys Ala Ser Asp Pro Thr 150 155 160	585
60	AGC ATC TCA CTT TCC TTG CTG GAC AAA CAC AGC CAA ATC ATC AAC AAG Ser Ile Ser Leu Ser Leu Leu Asp Lys His Ser Gln Ile Ile Asn Lys 165 170 175	633
65	TTC GTG AAT AGC GTG ATC AAC ACG CTG AAA AGC ACT GTA TCC TCC CTG Phe Val Asn Ser Val Ile Asn Thr Leu Lys Ser Thr Val Ser Ser Leu 180 185 190	681
70	CTG CAG AAG GAG ATA TGT CCA CTG ATC CGC ATC TTC ATC CAC TCC CTG Leu Gln Lys Glu Ile Cys Pro Leu Ile Arg Ile Phe Ile His Ser Leu 195 200 205	729
75	GAT GTG AAT GTC ATT CAG CAG GTC GTC GAT AAT CCT CAG CAC AAA ACC Asp Val Asn Val Ile Gln Gln Val Val Asp Asn Pro Gln His Lys Thr 210 215 220 225	777
80	CAG CTG CAA ACC CTC ATT TGAAGAGGAC GAATGAGGAG GACCACTGTG Gln Leu Gln Thr Leu Ile 230	825
85	GTGCATGCTG ATTGGTTCCC AGTGGCTTGC CCCACCCCT TATAGCATCT CCCTCCAGGA	885
90	AGCTGCTGCC ACCACCTAAC CAGCGTGAAA GCCTGAGTCC CACCAGAAGG ACCTTCCCAG	945

10020339121804

ATACCCCTTC TCCTCACAGT CAGAACAGCA GCCTCTACAC ATGTTGTCCT GCCCCTGGCA 1005
ATAAAGGCCC ATTTCTGCAA AAA 1028

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Gln Leu Trp Lys Leu Val Leu Leu Cys Gly Val Leu Thr Gly
-18 -15 -10 -5
Thr Ser Glu Ser Leu Leu Asp Asn Leu Gly Asn Asp Leu Ser Asn Val
1 5 10
Val Asp Lys Leu Glu Pro Val Leu His Glu Gly Leu Glu Thr Val Asp
15 20 25 30
Asn Thr Leu Lys Gly Ile Leu Glu Lys Leu Lys Val Asp Leu Gly Val
35 40 45
Leu Gln Lys Ser Ser Ala Trp Gln Leu Ala Lys Gln Lys Ala Gln Glu
50 55 60
Ala Glu Lys Leu Leu Asn Asn Val Ile Ser Lys Leu Leu Pro Thr Asn
65 70 75
Thr Asp Ile Phe Gly Leu Lys Ile Ser Asn Ser Leu Ile Leu Asp Val
80 85 90
Lys Ala Gly Pro Ile Asp Asp Gly Lys Gly Leu Asn Leu Ser Phe Pro
95 100 105 110
Val Thr Ala Asn Val Thr Val Ala Gly Pro Ile Ile Gly Gln Ile Ile
115 120 125
Asn Leu Lys Ala Ser Leu Asp Leu Leu Thr Ala Val Thr Ile Glu Thr
130 135 140
Asp Pro Gln Thr His Gln Pro Val Ala Val Leu Gly Glu Cys Ala Ser
145 150 155
Asp Pro Thr Ser Ile Ser Leu Ser Leu Leu Asp Lys His Ser Gln Ile
160 165 170
Ile Asn Lys Phe Val Asn Ser Val Ile Asn Thr Leu Lys Ser Thr Val
175 180 185 190
Ser Ser Leu Leu Gln Lys Glu Ile Cys Pro Leu Ile Arg Ile Phe Ile
195 200 205
His Ser Leu Asp Val Asn Val Ile Gln Gln Val Val Asp Asn Pro Gln
210 215 220
His Lys Thr Gln Leu Gln Thr Leu Ile
225 230

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
(B) TYPE: amino acid

10020139-121501

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met. Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly
 1          5          10          15
Asn Ser Glu Ser Leu Leu Gly Glu Leu Gly Ser Ala Val Asn Asn Leu
15          20          25          30
Lys Ile Leu Asn Pro Pro Ser Glu Ala Val Pro Gln Asn Leu Asn Leu
35          40          45
Asp Val Glu Leu Leu Gln Gln Ala Thr Ser Trp Pro Leu Ala Lys Asn
50          55          60
Ser Ile Leu Glu Thr Leu Asn Thr Ala Asp Leu Gly Asn Leu Lys Ser
65          70          75          80
Phe Thr Ser Leu Asn Gly Leu Leu Leu Lys Ile Asn Asn Leu Lys Val
85          90          95
Leu Asp Phe Gln Ala Lys Leu Ser Ser Asn Gly Asn Gly Ile Asp Leu
100         105         110
Thr Val Pro Leu Ala Gly Glu Ala Ser Leu Val Leu Pro Phe Ile Gly
115         120         125
Lys Thr Val Asp Ile Ser Val Ser Leu Asp Leu Ile Asn Ser Leu Ser
130         135         140
Ile Lys Thr Asn Ala Gln Thr Gly Leu Pro Glu Val Thr Ile Gly Lys
145         150         155         160
Cys Ser Ser Asn Thr Asp Lys Ile Ser Ile Ser Leu Leu Gly Arg Arg
165         170         175
Leu Pro Ile Ile Asn Ser Ile Leu Asp Gly Val Ser Thr Leu Leu Thr
180         185         190
Ser Thr Leu Ser Thr Val Leu Gln Asn Phe Leu Cys Pro Leu Leu Gln
195         200         205
Tyr Val Leu Ser Thr Leu Asn Pro Ser Val Leu Gln Gly Leu Leu Ser
210         215         220
Asn Leu Leu Ala Gly Gln Val Gln Leu Ala Leu
225         230         235

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly
1 5 10 15

5 Thr Ser Glu Ser Leu Leu Gly Asp Val Ala Asn Ala Val Asn Asn Leu
20 25 30

Asp Ile Leu Asn Ser Pro Ser Glu Ala Val Ala Gln Asn Leu Asn Leu
35 40 45

10 Asp Val Gly Ser Leu Gln Gln Ala Thr Thr Trp Pro Ser Ala Lys Asp
50 55 60

Ser Ile Leu Glu Thr Leu Asn Lys Val Glu Leu Gly Asn Ser Asn Gly
65 70 75 80

15 Phe Thr Pro Leu Asn Gly Leu Leu Leu Arg Val Asn Lys Phe Arg Val
85 90 95

20 Leu Asp Leu Gln Ala Gly Leu Ser Ser Asn Gly Lys Asp Ile Asp Leu
100 105 110

Lys Leu Pro Leu Val Phe Glu Ile Ser Phe Ser Leu Pro Val Ile Gly
115 120 125

25 Pro Thr Leu Asp Val Ala Val Ser Leu Asp Leu Leu Asn Ser Val Ser
130 135 140

Val Gln Thr Asn Ala Gln Thr Gly Leu Pro Gly Val Thr Leu Gly Lys
145 150 155 160

30 Cys Ser Gly Asn Thr Asp Lys Ile Ser Ile Ser Leu Leu Gly Arg Arg
165 170 175

35 Leu Pro Phe Val Asn Arg Ile Leu Asp Gly Val Ser Gly Leu Leu Thr
180 185 190

Gly Ala Val Ser Ile Leu Leu Gln Asn Ile Leu Cys Pro Val Leu Gln
195 200 205

40 Tyr Leu Leu Ser Thr Met Ser Gly Ser Ala Ile Gln Gly Leu Leu Ser
210 215 220

Asn Val Leu Thr Gly Gln Leu Ala Val Pro Leu
225 230 235

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear.

55 (ii) MOLECULE TYPE: protein

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly
1 5 10 15

65 Thr Ser Gly Ser Leu Phe Asp Ile Phe Gln Asn Pro Glu Leu Asp Val
20 25 30

Glu Ser Val Trp Ser Glu Ile Asn Tyr Arg Ile Arg Tyr Ala Leu Glu
35 40 45

10060139-121801

Thr Met Asp Leu Asp Met Leu Ala Asp Tyr Leu Ser Lys Arg Gly Ile
 50 55 60
 5 Glu Leu Lys Ile Lys Asp Leu Arg Ile Leu Asn Leu Asn His Glu Val
 65 70 75 80
 Ser Pro Asn Gly Asp Glu Val Thr Leu Lys Met Pro Met Ala Leu Asn
 85 90 95
 10 Ala Ser Leu Ser Leu Pro Ala Arg Asp Leu Thr Thr Asp Val Ser Ile
 100 105 110
 Ser Met Glu Ala Ile Thr Ser Phe Ala Ile Glu Lys Asp Pro Lys Thr
 115 120 125
 15 Gly Arg Arg Val Leu Asn Met Gln Arg Cys Ser Leu Asn Thr Asp Asn
 130 135 140
 Thr Ser Ile Ser Leu Leu Asn Arg Lys Ser Asn Phe Val Asn Leu Ala
 145 150 155 160
 Leu Asp Ser Ala Leu Tyr Leu Ile Lys Arg Gly Leu Thr Leu Pro Val
 165 170 175
 25 Arg Arg Gln Leu Cys Pro Val Leu Gln Leu Ile Ile Ser Asn Thr Phe
 180 185 190
 His Pro Asp Glu Ile Ser Asn Pro Gln Thr Ala Ile Ser Thr
 195 200 205

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTACAGCCAT GGAGTCTCTT CTTGACAATC TTGGCAATG

39

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CATCGCGGAT CCAATGAGGG TTGCGAGCTG GGTTTT

36

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid

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(ii) MOLECULE TYPE: DNA (genomic)

5	ATGAGCATCC TCCTCTAAAC GCGTGTCAAG ACAAAGATG CTNNCAGCTT TGGAAACTTG	60
	TTCTCCTGTG CGGCGTGCTC ACTGGGACCT CAGAGTCTCT TCTTGACAAT CTTGGCAATG	120
10	ACCTAAGCAA TGTCGTGGAT AAGCTGGAAC CTGTTCTTCA CGAGGGACTT GAGACAGTTG	180
	ACAATACTCT TAAAGGCATC CTTGAGAAAC TGAAGGTCGA CCTAGGAGTG CTTGAGAAAT	240
15	CCAGTGCTTG GCAACTGGCC AACAGAAGN CCAGGAAGCT GAGAAATTGC TGAACAATGT	300
	CATTTCTAAG CTGCTTCCAA CTAACACGGA CATTTTGGG TTGAAANTCA GCAATNCCCN	360
	CANCCGGATG TTCAAAGNTG NANCGATCGA TGATGGGCAA AGGCTTTAAN CCGGAGGCTT	420
20	CCCTGTTTAC CGGGAATGTT CAANGTNGGC CCGGGCCCN CATTTGGGCCA GNTTATCAAA	480
	NCTGGAAAGC TTCCTGGGAC CTCGGGACNG GNTCAACAAT TGAAANGATT CCCCAGANA	538

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

40	GGCACGAGAT TTCATGAGCA TCCTCCTCTA AACCGGTGTC AAGACAAAAG ATGCTTCAGC	60
	TTTGAAACT TGTTCTCCTG TCGCGCGTGC TCACTGGGAC CTCAGAGTCT CTTCTTGACA	120
	ATCTTGCAA TGACCTAAGC AATGTCGTGG ATAAGCTGGG AACCTGTTCT TCACGAGGGA	180
45	CTTGAGACAG TTGACAATAC TCTTAAAGGC ATCCTTGAGA AACTGAAGGT CGANCTAGGA	240
	GTGCTTCAGA AATCCAGTGC TTGGCAACTG GNCAAGCAGA AGGNCCCAGG AAGCTGAGAA	300
	ATTGCTGGAN CAATGTCAAT TCTAAGCTGN TTCCGACTAA CACGGNCATT TTTGGGTTG	359

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

65 ACCCACGCGT CCGGCGTGAT CAACACGCTG AAAAGCACTG TATCCTCCCT GCTGCAGAAG 60
GAGATATGTC CACTGATCCG CATCTTCATC CACTCCCTGG ATGTGAATGT CATTGAGCAG 120
GTCGTCGATA ATCCTCAGCA CAAAACCCAG CTGCAAACCC TCATCTGAAG AGGACGAATG 180

AGGAGGACCA CTGTGGTGCA TGCTGATTGG TTCCCACTGG CTTGCCCCAC CCCCTTATAG 240
 CATCTCCCTC CAGGAAGCTG CTGCCACCAC CTAACCAGCG TGAAAGCCTG GAGTCCCACC 300
 AGAAGGACCT TCCCAGATAC CCCTTTTTC TCACAGTCAG AGNGGNNGC CTCTTACACN 360
 TGTTGTCCNG GCCC 374

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTCATGAGCA TCCTCCTCTA AACGCGTGTC AAGACAAAAG ATGCTTCACT TTGGAAACTT 60
 GTTCTCCTGT GCGGCGTGCT CACTGGGACC TCAGAGTCTC TTCTTGACAA TCTTGGCAAT 120
 GACCTAAGCA ATGTCGTGGA TAAGCTGGAA CCTGTTCTTC ACGAGGGACT TGAGACAGTT 180
 GACAATACTC TTAAAGGCAT CCTTGAGAAA CTGAAGGTCG ACCTAGGAGT GCTTCAGAAA 240
 TCCAGTGCTT GGCAACTGGG CCANCAGAAA GGCCGAGGA AAGCGGAGAA ATTGCTGGAA 300
 CAATGTTTCT TTCTAAAGCT GCTTTCCAAC TAACACGGGA CNTTTTTGGG GTTTGNAAAA 360
 TCAGCCAAC TCCCTCAACC NNGGATGTTT CAAAGCTGGA AACCGN 406

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGACCCACG CGTCCGCCGC CCCCAACTTT TTGGCAGTTC TCCCATCTCT TGCCCACTTG 60
 ACCAGACTTT AATAGTTCCC TGTGTTTTCC AGACACAGCC AAATCATCAA CAAGTTCGTG 120
 AATAGCGTGA TCAACAGCCT GAAAAGCACT GTATCCTCCC TGCTGCAGAA GGAGATATGT 180
 CCACTGATCC GCATCTTCAT CCACTCCCTG GATGTGAATG TCATTCAGCA GGTCGTCGAT 240
 AATCCTCAGC AAAAAACCCA GCTGCAAACC CTCATCTGAA GAGGACGAAT GAGGAGGACC 300
 ACTGTGGTGC ATGCTGGTGA GGAGCCAGTC TCTGTGCCCC AATGCACAGG GGCCTATGGT 360
 GAAGTAAAAG TCAAGCGTGG CTTCCTTAT TTTTGTGTTA GAAGACTGTG CCTTCATCTC 420
 AGTCATAGAT TGAGCCCTGG NCCCCATCCC ANGCTAAGGC CTGATTCTGG TCANACTCTG 480

FOR SET "SEQUENCE"

493

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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TCGACCCACA	CGTCCGCGCTG	ACTGACAGAA	GGAGATATGT	CCATGATCCG	ACATTCTTAC	60
ATCCACTCCC	TGGATGTGAA	TGTTCAATTNC	AGCAGGTCGT	NCGATAATCC	NGCAGCACAA	120
AACCCAGCTG	GCAAACCCCTN	CATCTGAAGA	NGACGAATGA	GGANGACCAC	TGTGGGTGCA	180
TGCTGATTGG	TNTCCCACTG	GGCTTGCCCC	AACCCCTTA	NAGCANCTCC	CTCCAGGAAG	240
CTGCTGCNAA	CCAACCGAAC	CAGCGTGAAA	GCCTGAATNC	CACCAGAAGG	ACCTTCCCAG	300
ATANCCCTGC	TNCNCAACAG	TNAAGAACAG	CAGCTTCGAA	CAACATGNNG	TTCTGGCCCC	360
CGGGCAATAA	AAGGCCCAT	TTGGCAAAAA	AAAAA			395

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SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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GGCACGANAT TTCATGAGCA TCCTCCTCTA AACACGTGTC AAGACAAAAG ATGCTTCAGC 60

TTTGGNAACT TGTTCTCCTA TNCNGCGTGC TCACTGNGAC CTCAGAATCT CTNCTT 116

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(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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GTGGNCCGGG	GCCCATCATT	GGGCCAGANT	TATCAACCTG	AAAGCCTCCN	NGGANCTCCT	60
GACCGCAGTC	AACAATTGGA	AACTGGATCC	CCCAGAACAA	CAACCAGCCT	GGTTGNCCGT	120
NCTGGGGAAG	AATGCCGNCC	AATGAANCCC	AAACCAAGCA	NCTTCACTNN	TNCCTNGGCT	180
GGGGACCAAA	ACACCAGGCC	AAAATCCANT	NAANCAAGTN	TCCGTGGNAA	TAAGCGTGGA	240
ATCCAAACAA	CGCTGGGAAA	AAGCANTGGG	NATNCCNTCC	CTGGCTGGGC	AAGAAAGGGN	300
GATATGGTCC	ACTGGAATCC	GGAATTTTTA	ANCCAATTCC	CTNGGAATGT	GGNAATGTCA	360